

SEQUENCE LISTING

<110> Sumitomo Chemical Company Limited

<120> NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND
UTILIZATION THEREOF

<130>

<150> JP 2002/206841

<151> 2002-07-16

<150> JP 2002/367778

<151> 2002-12-19

<150> JP 2003/095955

<151> 2003-03-31

<160> 34

<210> 1

<211> 458

<212> PRT

<213> Homo sapiens

<400> 1

Met Gly Leu Cys Tyr Ser Leu Arg Pro Leu Leu Phe Gly Gly Pro Gly
 1 5 10 15
 Asp Asp Pro Cys Ala Ala Ser Glu Pro Pro Val Glu Asp Ala Gln Pro
 20 25 30
 Ala Pro Ala Pro Ala Leu Ala Pro Val Arg Ala Ala Ala Arg Asp Thr
 35 40 45
 Ala Arg Thr Leu Leu Pro Arg Gly Gly Glu Gly Ser Pro Ala Cys Ala
 50 55 60
 Arg Pro Lys Ala Asp Lys Pro Lys Glu Lys Arg Gln Arg Thr Glu Gln
 65 70 75 80
 Leu Ser Ala Glu Glu Arg Glu Ala Ala Lys Glu Arg Glu Ala Val Lys
 85 90 95
 Glu Ala Arg Lys Val Ser Arg Gly Ile Asp Arg Met Leu Arg Asp Gln
 100 105 110
 Lys Arg Asp Leu Gln Gln Thr His Arg Leu Leu Leu Leu Gly Ala Gly
 115 120 125
 Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His Val
 130 135 140
 Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu Asp Ile Arg
 145 150 155 160
 Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala Met Ser Thr
 165 170 175
 Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln Phe Arg Ser
 180 185 190
 Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu Tyr Ser Gln

195	200	205
Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu Gly Val Lys		
210	215	220
Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln		
225	230	235
Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp Tyr Thr Pro		
245	250	255
Thr Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe		
260	265	270
Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val		
275	280	285
Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp		
290	295	300
Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr Asn Met Val		
305	310	315
Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser Leu Asp Leu		
325	330	335
Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Ile Ile		
340	345	350
Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val Leu Ala Gly		
355	360	365
Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn Tyr Thr Val		
370	375	380
Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys Val Thr Arg		
385	390	395
		400

Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser Thr Ala Thr

405

410

415

Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp

420

425

430

Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln

435

440

445

Arg Met His Leu Lys Gln Tyr Glu Leu Leu

450

455

<210> 2

<211> 1377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1377)

<400> 2

atg ggt ctg tgc tac agt ctg cgg ccg ctg ctt ttc ggg ggc cca ggg 48

Met Gly Leu Cys Tyr Ser Leu Arg Pro Leu Leu Phe Gly Gly Pro Gly

1

5

10

15

gac gac ccc tgc gcg gcc tcg gag ccg ccg gtg gag gac gcg cag ccc 96

Asp Asp Pro Cys Ala Ala Ser Glu Pro Pro Val Glu Asp Ala Gln Pro

20

25

30

gcc ccg gcc ccg gcc ctg gcc cca gtc cgg gcg gcc gca agg gac acg 144

Ala Pro Ala Pro Ala Leu Ala Pro Val Arg Ala Ala Ala Arg Asp Thr

35

40

45

gcc cgg acc ctg ctc cct cgg ggc ggc gaa ggg agc ccg gca tgc gct 192

Ala Arg Thr Leu Leu Pro Arg Gly Gly Glu Gly Ser Pro Ala Cys Ala

50

55

60

cgg ccc aaa gca gac aag ccg aag gag aag cgg cag cgc acc gag cag 240

Arg Pro Lys Ala Asp Lys Pro Lys Glu Lys Arg Gln Arg Thr Glu Gln

65

70

75

80

ctg agt gcc gag gag cgc gag gcg gcc aag gag cgc gag gcg gtc aag 288

Leu Ser Ala Glu Glu Arg Glu Ala Ala Lys Glu Arg Glu Ala Val Lys

85

90

95

gag gcg agg aaa gtg agc cgg ggc atc gac cgc atg ctg cgc gac cag 336

Glu Ala Arg Lys Val Ser Arg Gly Ile Asp Arg Met Leu Arg Asp Gln

100

105

110

aag cgc gac ctg cag cag acg cac cgg ctc ctg ctg ctc ggg gct ggt 384

Lys Arg Asp Leu Gln Gln Thr His Arg Leu Leu Leu Leu Gly Ala Gly

115

120

125

gag tct ggg aaa agc acc atc gtc aaa cag atg agg atc ctg cac gtc 432

Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His Val

130

135

140

aat ggg ttt aat ccc gag gaa aag aaa cag aaa att ctg gac atc cgg 480

Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu Asp Ile Arg

145

150

155

160

aaa aat gtt aaa gat gct atc gtg aca att gtt tca gca atg agt act 528

Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala Met Ser Thr

165

170

175

ata ata cct cca gtt ccg ctg gcc aac cct gaa aac caa ttt cga tca 576

Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln Phe Arg Ser

180

185

190

gac tac atc aag agc ata gcc cct atc act gac ttt gaa tat tcc cag 624

Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu Tyr Ser Gln

195

200

205

gaa ttc ttt gac cat gtg aaa aaa ctt tgg gac gat gaa ggc gtg aag 672

Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu Gly Val Lys

210

215

220

gca tgc ttt gag aga tcc aac gaa tac cag ctg att gac tgt gca caa	720
Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln	
225 230 235 240	
tac ttc ctg gaa aga atc gac agc gtc agc ttg gtt gac tac aca ccc	768
Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp Tyr Thr Pro	
245 250 255	
aca gac cag gac ctc ctc aga tgc aga gtt ctg aca tct ggg att ttt	816
Thr Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe	
260 265 270	
gag aca cga ttc caa gtg gac aaa gta aac ttc cac atg ttt gat gtt	864
Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val	
275 280 285	
ggt ggc cag agg gat gag agg aga aaa tgg atc cag tgc ttt aac gat	912
Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp	
290 295 300	
gtc aca gct atc att tac gtc gca gcc tgc agt agc tac aac atg gtg	960
Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr Asn Met Val	
305 310 315 320	
att cga gaa gat aac aac acc aac agg ctg aga gag tcc ctg gat ctt	1008

Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser Leu Asp Leu

325

330

335

ttt gaa agc atc tgg aac aac agg tgg tta cgg acc att tct atc atc 1056

Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Ile Ile

340

345

350

ttg ttc ttg aac aaa caa gat atg ctg gca gaa aaa gtc ttg gca ggg 1104

Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val Leu Ala Gly

355

360

365

aaa tca aaa att gaa gac tat ttc cca gaa tat gca aat tat act gtt 1152

Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn Tyr Thr Val

370

375

380

cct gaa gac gca aca cca gat gca gga gaa gat ccc aaa gtt aca aga 1200

Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys Val Thr Arg

385

390

395

400

gcc aag ttc ttt atc cgg gac ctg ttt ttg agg atc agc acg gcc acc 1248

Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser Thr Ala Thr

405

410

415

ggc gac ggc aaa cat tac tgc tac ccg cac ttc acc tgc gcc gtg gac 1296

Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp

420

425

430

aca gag aac atc cgc agg gtg ttc aac gac tgc cgc gac atc atc cag 1344

Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln

435

440

445

cgg atg cac ctc aag cag tat gag ctc ttg tga

1377

Arg Met His Leu Lys Gln Tyr Glu Leu Leu

450

455

<210> 3

<211> 44

<212> RNA

<213> artificial sequence

<220>

<223> an example of the ribozyme of the present invention

<400> 3

tcgcctcctt ctgatgaggc cgaaaggccg aaaccgcctc gcgc

44

<210> 4

<211> 44

<212> RNA

<213> artificial sequence

<220>

<223> an example of the ribozyme of the present invention

<400> 4

cggccgcccc ctgatgaggc cgaaaggccg aaactggggc cagc

44

<210> 5

<211> 43

<212> RNA

<213> artificial sequence

<220>

<223> an example of the ribozyme of the present invention

<400> 5

cagcggccgc ctgatgaggc cgaaaggccg aaactgtagc aca

43

<210> 6

<211> 54

<212> RNA

<213> artificial sequence

<220>

<223> an example of the ribozyme of the present invention

<400> 6

tcgcctcctt agaagcctac cagagaaaca cacgttgtgg tatattacct ggta 54

<210> 7

<211> 54

<212> RNA

<213> artificial sequence

<220>

<223> an example of the ribozyme of the present invention

<400> 7

cggccgccccg agaaggggac cagagaaaca cacgttgtgg tatattacct ggta 54

<210> 8

<211> 55

<212> RNA

<213> artificial sequence

<220>

<223> an example of the ribozyme of the present invention

<400> 8

cagcggccgc aagaagtaga ccagagaaac acacgttgtg gtatattacc tggtta 55

<210> 9

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> an example of the oligonucleotide of the present invention

<400> 9

atgggtctgt gctacagtct gcgg

24

<210> 10

<211> 37

<212> DNA

<213> artificial sequence

<220>

<223> an example of the oligonucleotide of the present invention

<400> 10

acgatggtgc ttttcccaga ctcaccagcc ccgagca

37

<210> 11

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 11

atgggtctgt gctacagtct gcgg

24

<210> 12

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 12

tcacaagagc tcatactgct t

21

<210> 13

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 13

atggggtgtt tgggcggcaa ca

22

<210> 14

<211> 37

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 14

acgatggtgc ttttcccaga ctcaccagcc ccgagca

37

<210> 15

<211> 29

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 15

atgggcctat gctacagcct gcggccgct

29

<210> 16

<211> 36

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 16

gctgcaggtc ccgcttctgc tcgcgcagca tgcggt

36

<210> 17

<211> 36

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 17

agctcggatc catgaggact ctgaacacct ctgcca

36

<210> 18

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 18

gtgcagaatt ctcatctgcg agttcaggtt ggg

34

<210> 19

<211> 40

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 19

agctcggatc catggatcca ctgaatctgt cctggtatga

40

<210> 20

<211> 41

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 20

gtgcagaatt ctcagcagtg aaggatcttc tggaaggcct t

41

<210> 21

<211> 26

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 21

atgagtgagc ttgaccagtt acggca

26

<210> 22

<211> 26

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 22

ttagttccag atcttgagga agctat

26

<210> 23

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 23

atgaaagggtg agaccccggt gaaca

25

<210> 24

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> a primer used in an example of the present invention

<400> 24

tcagaggaga gcacagaaga actt

24

<210> 25

<211> 448

<212> PRT

<213> Mus musculus

<400> 25

Met Gly Leu Cys Tyr Ser Leu Arg Pro Leu Leu Phe Gly Ser Pro Glu

1 5 10 15

Asp Thr Pro Cys Ala Ala Ser Glu Pro Cys Ala Glu Asp Ala Gln Pro

20 25 30

Ser Ala Ala Pro Ala Pro Ala Ser Ile Pro Ala Pro Ala Pro Val Gly

35 40 45

Thr Leu Leu Arg Arg Gly Gly Gly Arg Ile Val Ala Asn Ala Arg Pro

50 55 60

Pro Gly Glu Leu Gln Ser Arg Arg Arg Gln Glu Gln Leu Arg Ala Glu

65 70 75 80

Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly Ile Asp

85 90 95

Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His Arg Leu

100 105 110

Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln

115 120 125

Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln

130	135	140	
Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Ile Val Thr Ile			
145	150	155	160
Val Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala Asn Pro			
	165	170	175
Glu Asn Gln Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr			
	180	185	190
Asp Phe Glu Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys Leu Trp			
	195	200	205
Asp Asp Glu Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln			
	210	215	220
Leu Ile Asp Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser			
225	230	235	240
Leu Val Asp Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys Arg Val			
	245	250	255
Leu Thr Ser Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys Val Asn			
	260	265	270
Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp			
	275	280	285
Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala Ala Cys			
	290	295	300
Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu			
305	310	315	320
Arg Glu Ser Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu			
	325	330	335

Arg Thr Ile Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met Leu Ala

340

345

350

Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu

355

360

365

Tyr Ala Asn Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu

370

375

380

Asp Pro Lys Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu

385

390

395

400

Arg Ile Ser Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr Pro His

405

410

415

Phe Thr Cys Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe Asn Asp

420

425

430

Cys Arg Asp Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu Leu Leu

435

440

445

<210> 26

<211> 450

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Gly Leu Cys Tyr Ser Leu Arg Pro Leu Leu Phe Gly Ser Ser Gly

1

5

10

15

Asp Ala Pro Cys Glu Asp Ser Glu Pro Cys Ala Glu Asp Ala Gln Pro

20

25

30

Ser Ala Ala Pro Ala Pro Ala Pro Ala Pro Ile Pro Ala Pro Ala Pro

35

40

45

Val Gly Thr Leu Leu Arg Arg Gly Asp Gly Arg Ile Pro Ala Ser Ala

50

55

60

Arg Ser Pro Val Glu Leu Gln Asn Arg Arg Arg Gln Glu Gln Leu Arg

65

70

75

80

Ala Glu Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly

85

90

95

Ile Asp Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His

100

105

110

Arg Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val

115

120

125

Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys

130

135

140

Lys Gln Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Leu Val

145

150

155

160

Thr Ile Ile Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala

165

170

175

Asn Pro Glu Asn Gln Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro

180

185

190

Ile Thr Asp Phe Glu Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys

195

200

205

Leu Trp Asp Asp Glu Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu

210

215

220

Tyr Gln Leu Ile Asp Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser

225	230	235	240
Val Ser Leu Val Asp Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys			
	245	250	255
Arg Val Leu Thr Ser Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys			
	260	265	270
Val Asn Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg			
	275	280	285
Lys Trp Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala			
	290	295	300
Ala Cys Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn			
305	310	315	320
Arg Leu Arg Glu Ser Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg			
	325	330	335
Trp Leu Arg Thr Ile Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met			
	340	345	350
Leu Ala Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe			
	355	360	365
Pro Glu Tyr Ala Asn Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala			
	370	375	380
Gly Glu Asp Pro Lys Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu			
385	390	395	400
Phe Leu Arg Ile Ser Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr			
	405	410	415
Pro His Phe Thr Cys Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe			
	420	425	430

Asn Asp Cys Arg Asp Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu

435

440

445

Leu Leu

450

<210> 27

<211> 1347

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1347)

<400> 27

atg ggc cta tgc tac agc ctg cgg ccg ctg ctc ttc ggg agc cca gag 48

Met Gly Leu Cys Tyr Ser Leu Arg Pro Leu Leu Phe Gly Ser Pro Glu

1

5

10

15

gac acc ccg tgt gcg gcc tcg gaa ccc tgc gca gag gat gct cag ccc 96

Asp Thr Pro Cys Ala Ala Ser Glu Pro Cys Ala Glu Asp Ala Gln Pro

20

25

30

agc gcc gcc ccg gcc cct gcc tcg atc cca gcc ccg gct ccc gta ggg 144

Ser Ala Ala Pro Ala Pro Ala Ser Ile Pro Ala Pro Ala Pro Val Gly

35

40

45

acc ctg ctc cgg cgt ggc ggc ggc cgg atc gtc gcg aac gcg cgg ccg 192

Thr Leu Leu Arg Arg Gly Gly Gly Arg Ile Val Ala Asn Ala Arg Pro

50

55

60

cca ggc gag ctg cag agc cgc cgg cga cag gag cag cta cga gcc gag 240

Pro Gly Glu Leu Gln Ser Arg Arg Arg Gln Glu Gln Leu Arg Ala Glu

65

70

75

80

gag cgc gag gcg gct aaa gag gcg agg aaa gtc agc cgg ggc atc gac 288

Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly Ile Asp

85

90

95

cgc atg ctg cgc gag cag aag cgg gac ctg cag cag acg cac cgg ctc 336

Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His Arg Leu

100

105

110

ctg ctg ctg ggg gct ggt gag tcc ggg aaa agc act atc gtc aaa cag 384

Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln

115

120

125

atg agg atc ctg cac gtc aat ggc ttc aac ccc gag gaa aag aag cag 432

Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln

130

135

140

aaa att ctg gac atc agg aaa aat gtc aaa gat gcg atc gtg aca atc 480

Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Ile Val Thr Ile

145 150 155 160

gtt tca gca atg agt act atc ata cct cca gtt cca ctg gcc aac cct 528

Val Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala Asn Pro

165 170 175

gag aac cag ttc cgg tca gat tat atc aag agc ata gcc cct atc act 576

Glu Asn Gln Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr

180 185 190

gac ttt gaa tat tcc cag gag ttc ttt gac cat gtg aag aag ctg tgg 624

Asp Phe Glu Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys Leu Trp

195 200 205

gac gat gaa gga gtg aag gcc tgc ttt gag aga tcc aac gag tac cag 672

Asp Asp Glu Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln

210 215 220

ctg atc gac tgt gca caa tac ttc ctg gaa agg att gac agt gtc agt 720

Leu Ile Asp Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser

225 230 235 240

ctg gtt gac tac aca ccc aca gac cag gac ctg ctc aga tgc aga gtg 768

Leu Val Asp Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys Arg Val

245

250

255

ctg aca tca gga atc ttt gag aca cga ttc caa gtg gac aaa gtg aac 816

Leu Thr Ser Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys Val Asn

260

265

270

ttt cac atg ttt gat gtt gga ggc cag aga gat gag aga aga aaa tgg 864

Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp

275

280

285

atc cag tgt ttt aat gat gtc act gcg atc att tac gtg gcg gcc tgt 912

Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala Ala Cys

290

295

300

agt agc tac aac atg gtg atc cgg gaa gat aac aat acc aac aga ctt 960

Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu

305

310

315

320

cgg gaa tca ctg gac ctg ttt gaa agc atc tgg aat aac agg tgg ttg 1008

Arg Glu Ser Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu

325

330

335

cga acc att tct atc atc cta ttc ttg aac aaa caa gac atg ctg gca 1056

Arg Thr Ile Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met Leu Ala

340

345

350

gaa aaa gtc ttg gca ggg aag tca aaa atc gaa gac tat ttc ccg gag 1104

Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu

355

360

365

tat gcc aat tat act gtc cct gaa gat gca aca cca gat gcg gga gaa 1152

Tyr Ala Asn Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu

370

375

380

gat ccc aaa gtt aca aga gca aag ttc ttt atc cgg gat ctg ttc ttg 1200

Asp Pro Lys Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu

385

390

395

400

agg atc agc aca gcc acg ggt gat ggc aaa cat tac tgc tac cct cac 1248

Arg Ile Ser Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr Pro His

405

410

415

ttc acc tgc gcc gtg gac aca gag aac atc cgc aga gtg ttc aac gat 1296

Phe Thr Cys Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe Asn Asp

420

425

430

tgc cgt gac atc atc cag aga atg cat ctc aag cag tac gaa ctc ttg 1344

Cys Arg Asp Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu Leu Leu

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tga

1347

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<211> 1353

<212> DNA

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1

5

10

15

gac gcc ccc tgt gag gac tct gag ccg tgc gct gag gat gct cag ccc 96

Asp Ala Pro Cys Glu Asp Ser Glu Pro Cys Ala Glu Asp Ala Gln Pro

20

25

30

agc gcc gcc ccg gcc ccg gcc ccg gcc ccg atc cca gcc ccg gct ccg 144

Ser Ala Ala Pro Ala Pro Ala Pro Ala Pro Ile Pro Ala Pro Ala Pro

35

40

45

gtg ggg acc ctg ctc cgg cga ggc gac ggc cgg atc ccc gca agc gcg 192

Val Gly Thr Leu Leu Arg Arg Gly Asp Gly Arg Ile Pro Ala Ser Ala

50

55

60

agg tcg cca gtc gag ctg cag aac cgc cgg cga cag gag cag ctg cga 240

Arg Ser Pro Val Glu Leu Gln Asn Arg Arg Arg Gln Glu Gln Leu Arg

65

70

75

80

gcc gag gag cgc gag gca gct aag gag gcg agg aaa gta agc cgg ggt 288

Ala Glu Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly

85

90

95

atc gac cgc atg ctg cgc gaa cag aag cgc gac ctg cag cag acg cac 336

Ile Asp Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His

100

105

110

cgg ctc ctg ctc ttg ggg gct ggt gag tcc ggg aaa agc act ata gtc 384

Arg Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val

115

120

125

aaa cag atg agg atc cta cac gtc aat ggc ttc aac ccc gag gaa aag 432

Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys

130

135

140

aag cag aaa att ctg gac atc agg aaa aat gtc aaa gat gct tta gtg 480

Lys Gln Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Leu Val

145 150 155 160

aca atc att tca gca atg agt acc ata ata cct cca gtt cca ctg gcc 528

Thr Ile Ile Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala

165 170 175

aac cct gag aac cag ttt cgg tca gat tac atc aag agc ata gcc cct 576

Asn Pro Glu Asn Gln Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro

180 185 190

atc act gac ttt gaa tat tcc cag gag ttc ttt gac cac gtg aag aag 624

Ile Thr Asp Phe Glu Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys

195 200 205

ctg tgg gat gat gag gga gtg aag gcc tgc ttt gag aga tcc aac gag 672

Leu Trp Asp Asp Glu Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu

210 215 220

tac cag ctg atc gac tgt gca caa tac ttc ctg gaa agg att gac agc 720

Tyr Gln Leu Ile Asp Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser

225 230 235 240

gtg agt ctg gtt gac tac aca ccc aca gac cag gac cta ctc aga tgc 768

Val Ser Leu Val Asp Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys

245

250

255

aga gtg ctg aca tca ggg atc ttt gag aca cga ttc caa gtg gac aaa 816

Arg Val Leu Thr Ser Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys

260

265

270

gtg aac ttt cac atg ttt gac gtt gga ggc cag agg gat gag aga aga 864

Val Asn Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg

275

280

285

aaa tgg atc cag tgt ttt aac gat gtc act gcc atc atc tat gtg gca 912

Lys Trp Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala

290

295

300

gcc tgc agc agc tac aac atg gtg atc cgg gaa gat aac aac acc aac 960

Ala Cys Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn

305

310

315

320

aga ctc cgg gag tcg ctg gac ctg ttt gaa agc atc tgg aat aac agg 1008

Arg Leu Arg Glu Ser Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg

325

330

335

tgg tta cga acc att tcc atc atc ctg ttc ttg aac aaa caa gat atg 1056

Trp Leu Arg Thr Ile Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met

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ctg gca gaa aaa gtc ttg gcc ggg aag tca aaa att gaa gac tat ttc	1104		
Leu Ala Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe			
355	360	365	
ccg gag tat gcc aac tat act gtc cct gaa gat gca aca cca gat gca	1152		
Pro Glu Tyr Ala Asn Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala			
370	375	380	
gga gaa gat ccc aaa gtt aca aga gcc aag ttc ttt atc cgg gat ctg	1200		
Gly Glu Asp Pro Lys Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu			
385	390	395	400
ttc ttg agg atc agc aca gcc acg ggt gat ggc aaa cat tac tgc tac	1248		
Phe Leu Arg Ile Ser Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr			
405	410	415	
cct cac ttc acc tgc gcc gtg gac aca gag aac atc cgc aga gtg ttc	1296		
Pro His Phe Thr Cys Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe			
420	425	430	
aac gat tgt cgt gac atc atc cag aga atg cac ctc aag cag tac gaa	1344		
Asn Asp Cys Arg Asp Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu			
435	440	445	

ctc ttg tga

1353

Leu Leu

450

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33

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37

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34